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## Genetic testing and counseling among patients with newly diagnosed breast cancer

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## INTRODUCTION

Germline genetic testing of breast cancer patients is an important model of how increasingly widespread genomic sequencing can influence treatment decision-making. Testing of two breast cancer-associated genes, *BRCA1/2*, has been available for twenty years, but new massively parallel sequencing technology and less restrictive patent laws have made multiplex panel tests available at much lower costs.<sup>1</sup> Yet little is known about recent patient experience with genetic testing and counseling. Genetic counselors are expert in risk assessment and communication, but because of workforce limitations, some physicians must counsel and test patients without their assistance.<sup>2</sup> These challenges motivated this investigation of patients' use of and perspectives on genetic counseling and testing.

## METHODS

The study was approved by the University of Michigan Institutional Review Board, which waived the requirement of signed informed consent. Women aged 20 through 79 years, diagnosed with stages 0–II breast cancer between July 2013 and September 2014, identified by Surveillance Epidemiology and End Results registries of Georgia and Los Angeles County, were mailed surveys (Supplement) two months after surgery. Questions addressed how much patients wanted genetic testing (not at all, a little bit, somewhat, quite a bit, very much: the latter 4 were defined as wanting testing); and whether patients talked about testing

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with any “doctor or other health professional”, had a session with a genetic counseling expert, and/or had testing. Cancer family history, ancestry and clinical information were used to construct a guideline-concordant measure of high pre-test risk for mutation carriage.<sup>3</sup> A log-linear model was constructed (SAS Version 9.4, SAS Institute) to compute risk ratios, adjusting for covariates (listed in Table 1), and weighted for survey design and non response to identify variables independently associated with failure to receive testing among high-risk patients.

## RESULTS

A total of 2,529 women (71%) responded to the survey. The mean age was 62 years (standard deviation 11); 56.8% were white, 17.8% black, and 71.2% had some college education (Table 1). Sixty-six percent (95% CI, 64.2%–68.2%) reported wanting testing and 29.0% (95% CI, 27.1%–30.9%) reported having a test. Thirty-one percent (N=773, 95% CI, 29.2%–33.1%) of patients had high pre-test mutation risk. Among average-risk patients, 59.3% (95% CI, 56.8%–61.8%) wanted testing, 35.9% (95% CI, 33.4%–38.3%) reported talking about testing with any doctor/health professional, and 17.8% (95% CI, 16.0%–19.9%) had testing (Table 2). Among high-risk patients, 80.9% (95% CI, 78.0%–83.9%) wanted testing, 70.9% (95% CI, 67.5%–74.3%) talked about testing with any doctor/health professional, 39.6% (95% CI, 35.9%–43.3%) had a session with a genetic counseling expert, and 52.9% (95% CI, 49.1%–56.6%) had testing. Of tested high-risk patients, 61.7% (95% CI, 56.6%–66.7%) had an expert genetic counseling session. The most common reason high-risk patients reported for not testing was “my doctor didn’t recommend it” (56.1%), “too expensive” (13.7%), “I did not want it” (10.7%), and “my family didn’t want me to get it” (0.2%). On multivariable analysis (Table 1), characteristics associated with no testing included older age and Asian ethnicity but not education, income, or insurance.

## DISCUSSION

In this large, population-based study, most patients reported wanting genetic testing and 29% reported having it. Yet only 39.6% of all high-risk women and 61.7% of tested high-risk women reported having a genetic counseling session. This suggests a gap between need and availability of genetic counseling. Only 52.9% of high-risk patients had a genetic test, representing a missed opportunity to prevent ovarian and other cancer deaths among mutation carriers and their families. High-risk patients most vulnerable to under-testing included Asians and older women, despite evidence that many such patients carry mutations.<sup>4,5</sup>

Clinical need for genetic testing may not be adequately recognized by physicians. High-risk patients reported lack of a physician’s recommendation, not expense, as their primary reason for not testing. Limitations of the study include the testing data source being by patient self-report and that the patients lived in only 2 geographic regions. The findings emphasize the importance of cancer physicians in the genetic testing process. Priorities include improving physicians’ communication skills and assessments of patients’ risk and desire for testing, and optimizing triage to genetic counselors.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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## References

1. Kurian AW, Ford JM. Multigene Panel Testing in Oncology Practice: How Should We Respond? *JAMA Oncol.* Jun 1; 2015 1(3):277–278. [PubMed: 26181167]
2. Delikurt T, Williamson GR, Anastasiadou V, Skirton H. A systematic review of factors that act as barriers to patient referral to genetic services. *Eur J Hum Genet.* Jun; 2015 23(6):739–745. [PubMed: 25205405]
3. Daly MB, Pilarski R, Axilbund JE, et al. Genetic/Familial High-Risk Assessment: Breast and Ovarian, Version 2.2015. *J Natl Compr Canc Netw.* Feb; 2016 14(2):153–162. [PubMed: 26850485]
4. Kurian AW, Gong GD, Chun NM, et al. Performance of BRCA1/2 mutation prediction models in Asian Americans. *J Clin Oncol.* Oct 10; 2008 26(29):4752–4758. [PubMed: 18779604]
5. Tung N, Lin NU, Kidd J, et al. Frequency of Germline Mutations in 25 Cancer Susceptibility Genes in a Sequential Series of Patients With Breast Cancer. *J Clin Oncol.* Mar 14.2016

Table 1

Distributions of Patient Characteristics Among All Patients\* and High-Risk<sup>a</sup> Patients Only and Associations With Non-Receipt of Genetic Testing Among High-Risk Patients

| Characteristic <sup>b</sup>                                 | All Patients |         | High-Risk Patients Only                                     |      |         |   | RR of no test (adjusted) <sup>e</sup>                   |
|---|--------------|---------|---|------|---------|---|---|
|   | N            | % or SD | Weighted <sup>c</sup> Mean or % and 95% confidence interval | N    | % or SD | Weighted <sup>c</sup> Mean or % and 95% confidence interval | Relative risk (RR) of no test (unadjusted) <sup>d</sup> |
| Age at survey administration, years (RR per +1 year of age) |              |         |   |      |         |   |   |
| Mean  | 61.9         | 11      | 62.0  | 58.6 | 13      | 58.9  | 1.04 (1.03 – 1.04)                                      |
| Race/Ethnicity <sup>f</sup>                                 |              |         |   |      |         |   |   |
| Non-Hispanic White  | 1350         | 53.4    | 56.8 (54.7 – 58.8)  | 406  | 52.5    | 55.9 (52.2 – 59.6)  | 1 (reference)   |
| Non-Hispanic Black  | 445          | 17.6    | 17.8 (16.2 – 19.4)  | 134  | 17.3    | 17.6 (14.7 – 20.5)  | 1.14 (0.94 – 1.39)                                      |
| Hispanic  | 442          | 17.5    | 13.9 (12.6 – 15.3)  | 140  | 18.1    | 14.7 (12.2 – 17.1)  | 0.97 (0.76 – 1.10)                                      |
| Asian   | 222          | 8.8     | 8.9 (7.7 – 10.0)  | 69   | 8.9     | 8.8 (6.8 – 10.9)  | 1.10 (0.85 – 1.43)                                      |
| Missing   | 70           | 2.8     | 2.7 (2.0 – 3.3)   | 24   | 3.1     | 3.0 (1.8 – 4.3)   | 1.39 (1.04 – 1.85)                                      |
| Education   |              |         |   |      |         |   |   |
| High school or less   | 750          | 29.5    | 27.7 (25.9 – 29.6)  | 224  | 29.0    | 26.7 (23.4 – 29.9)  | 1 (reference)   |
| At least some college                                       | 1752         | 69.3    | 71.2 (69.3 – 73.0)  | 539  | 69.7    | 72.2 (68.9 – 75.5)  | 0.73 (0.62 – 0.86)                                      |
| Missing   | 30           | 1.2     | 1.1 (0.7 – 1.5)   | 10   | 1.3     | 1.1 (0.4 – 1.9)   |   |
| Insurance status  |              |         |   |      |         |   |   |
| Private   | 1309         | 51.8    | 52.7 (50.7 – 54.8)  | 416  | 53.8    | 54.6 (50.9 – 58.4)  | 1 (reference)   |
| Medicaid / other public                                     | 385          | 15.2    | 14.2 (12.8 – 15.6)  | 125  | 16.2    | 15.1 (12.5 – 17.7)  | 1.35 (1.08 – 1.69)                                      |
| Medicare  | 722          | 28.6    | 28.8 (26.9 – 30.7)  | 190  | 24.6    | 25.1 (21.8 – 28.4)  | 1.82 (1.54 – 2.14)                                      |
| None  | 13           | 0.5     | 0.6 (0.2 – 0.9)   | 5    | 0.6     | 0.8 (0.1 – 1.6)   |   |
| Missing   | 100          | 4.0     | 3.7 (2.9 – 4.4)   | 37   | 4.8     | 4.4 (2.9 – 5.9)   |   |
| Income of household   |              |         |   |      |         |   |   |
| \$90,000 or more  | 615          | 24.3    | 25.8 (23.9 – 27.6)  | 195  | 25.2    | 27.8 (24.4 – 31.3)  | 1 (reference)   |
| \$40,000–\$89,999   | 682          | 27.0    | 27.8 (25.9 – 29.7)  | 193  | 25.0    | 25.4 (22.1 – 28.7)  | 1.29 (1.02 – 1.64)                                      |
| Less than \$40,000  | 776          | 30.7    | 29.3 (27.5 – 31.2)  | 240  | 31.0    | 28.6 (25.3 – 32.0)  | 1.58 (1.28 – 1.95)                                      |
| Missing   | 456          | 18.0    | 17.1 (15.6 – 18.7)  | 145  | 18.8    | 18.1 (15.2 – 20.9)  |   |
| Cancer stage  |              |         |   |      |         |   |   |

| Characteristic <sup>b</sup> | All Patients |         | High-Risk Patients Only                                     |     |         |   | Relative risk (RR) of no test (unadjusted) <sup>d</sup> | RR of no test (adjusted) <sup>e</sup> |
|-----------------------------|--------------|---------|---|-----|---------|---|---|---------------------------------------|
|                             | N            | % or SD | Weighted <sup>c</sup> Mean or % and 95% confidence interval | N   | % or SD | Weighted <sup>c</sup> Mean or % and 95% confidence interval |   |                                       |
| 0                           | 489          | 19.3    | 26.4 (24.4 – 28.4)  | 183 | 23.7    | 30.3 (26.6 – 34.0)  | 1 (reference)   | 1 (reference)                         |
| I–II                        | 1962         | 77.6    | 71.2 (69.1 – 73.2)  | 590 | 76.3    | 69.7 (66.0 – 73.4)  | 0.91 (0.78 – 1.08)                                      | 0.95 (0.85 – 1.06)                    |
| Missing                     | 78           | 3.1     | 2.5 (1.9 – 3.0)   | 0   | 0       | 0   |   |                                       |

<sup>a</sup>We selected 3,880 women diagnosed with early-stage breast cancer in 2013–2014; among them, 249 were ineligible due to having a prior breast cancer diagnosis or stages III–IV; residing outside the SEER registry area; or being deceased, too ill or unable to complete a survey in Spanish or English. Of 3,631 eligible women remaining, 1,053 could not be contacted or did not participate. Of 2,578 patients who responded (71%), 49 were ineligible because of genetic testing before their diagnosis, leaving 2,529 for the study sample.

<sup>b</sup>Patients were categorized as high-risk if they had one or more of the following: age at breast cancer diagnosis ≥ 45 years; bilateral breast cancer; triple-negative breast cancer diagnosed at age <60; any relative with: ovarian cancer, sarcoma, or male breast cancer; 2 first-degree relatives with breast cancer; for patients diagnosed at age 50, 1 first-degree relative with breast cancer; Ashkenazi Jewish ancestry; or family history of a deleterious genetic mutation (*BRCA1/2* or another mutation associated with increased breast cancer risk, e.g., *TP53*). All other patients were categorized as average risk.

<sup>c</sup>Patients provided information on race/ethnicity, family cancer history, insurance, education and income; SEER registries provided information on age, cancer stage, and biomarkers (estrogen and progesterone receptors, HER2).

<sup>d</sup>Survey design and non-response weights were created to compensate for the differential probability of selecting patients by race, stage and SEER site and to adjust for survey non-response. The weights were normalized to equal the observed sample size and all analyses are weighted.

<sup>e</sup>Univariate log-linear models were corrected for multiple imputation.

<sup>f</sup>Multivariable log-linear model (Poisson distribution with log link) corrected for multiple imputation and using robust standard error estimation were used. Survey and SEER item non-response was low (<4%) for most covariates and higher for self-reported income (17%). To correct for potential non-response bias, values for missing items were imputed using sequential multiple imputation (SMI). Results were compared between SMI analyses and complete-case analyses for any meaningful differences.

<sup>g</sup>Race/ethnicity were self-reported by the individuals according to the following options provided by the investigators: “White, Black or African-American, Native Hawaiian or other Pacific Islander, Asian Indian, Chinese, Filipino, Japanese, Korean, Vietnamese, Other Asian (please explain), Other Race (please explain)”. Race/ethnicity was assessed because of past studies that have reported differences in access to genetic testing according to race/ethnicity.

Table 2

Patient Preferences and Experiences of Genetic Testing

| Preferences and experiences             | High-risk <sup>a</sup> patients |             | Average-risk <sup>d</sup> patients |             |
|---|---------------------------------|-------------|------------------------------------|-------------|
|   | Weighted <sup>c</sup> %         | 95% CI      | Weighted <sup>c</sup> %            | 95% CI      |
| Wanted testing                          | 80.9                            | 78.0 – 83.9 | 59.3                               | 56.8 – 61.8 |
| Talked with any clinician about testing | 70.9                            | 67.5 – 74.3 | 35.9                               | 33.4 – 38.3 |
| Talked with genetic counselor           | 39.6                            | 35.9 – 43.3 | 14.4                               | 12.6 – 16.2 |
| Had genetic testing                     | 52.9                            | 49.1 – 56.6 | 17.8                               | 16.0 – 19.9 |

<sup>a</sup>Patients were categorized as high-risk if they had one or more of the following: age at breast cancer diagnosis < 45 years; bilateral breast cancer; triple-negative breast cancer diagnosed at age <60; any relative with: ovarian cancer, sarcoma, or male breast cancer; 2 first-degree relatives with breast cancer; for patients diagnosed at age 50, 1 first-degree relative with breast cancer; Ashkenazi Jewish ancestry; or family history of a deleterious genetic mutation (*BRCA1/2* or another mutation associated with increased breast cancer risk, e.g., *TP53*). All other patients were categorized as average risk.

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